OIPE IAP2 OCT 27 2005 PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Johnson, Leslie S.

Li, Hua

Tuaillon, Nadine

<120> SOLUBLE FCgammaR FUSION PROTEINS AND METHODS OF USE THEREOF

<130> 11183-005-999

<140> 10/756,153

<141> 2004-01-13

<150> 60/439,709

<151> 2003-01-13

<160> 54

<170> FastSEQ version 4.0

<210> 1

<211> 420

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIa-G2

<400> 1

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Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
            20                  25                  30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
        35                  40                  45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
    50                  55                  60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65                  70                  75                  80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
                85                  90                  95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His
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            100                 105                 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly
        115                 120                 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
    130                 135                 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly
145                 150                 155                 160

Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln Gly
                165                 170                 175

Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln Val
            180                 185                 190

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
        195                 200                 205

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
    210                 215                 220

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
225                 230                 235                 240

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
                245                 250                 255

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
            260                 265                 270

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
        275                 280                 285

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
    290                 295                 300

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
305                 310                 315                 320

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
                325                 330                 335

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
            340                 345                 350

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
        355                 360                 365

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
    370                 375                 380

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
385                 390                 395                 400

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
                405                 410                 415

Ser Pro Gly Lys
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420

<210> 2

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIb-G2

<400> 2

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1               5                  10                  15

Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr
            20                  25                  30

His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu
        35                  40                  45

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn
    50                  55                  60

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp
65                  70                  75                  80

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro
                85                  90                  95

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser
            100                 105                 110

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys
        115                 120                 125

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala
    130                 135                 140

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr
145                 150                 155                 160

Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser
                165                 170                 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
            180                 185                 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        195                 200                 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    210                 215                 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
225                 230                 235                 240
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Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
245 250 255

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
275 280 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
340 345 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<210> 3

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIa(131R)-G2

<400> 3

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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser
165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
210 215 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
225 230 235 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
245 250 255

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
260 265 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
275 280 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
290 295 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305 310 315 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
325 330 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
340 345 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
355 360 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
370 375 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln

385 390 395 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys
405

<210> 4

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIa(131H)-G2

<400> 4

Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro Trp Ile Asn Val
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Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly Ala Arg Ser Pro
20 25 30

Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr
35 40 45

His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly
50 55 60

Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His
65 70 75 80

Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu
85 90 95

Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp
100 105 110

Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys
115 120 125

Phe Ser His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser
130 135 140

His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
145 150 155 160

Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro Ser Met Gly Ser
165 170 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
180 185 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
195 200 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

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    210                 215                 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
225                 230                 235                 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                245                 250                 255

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
            260                 265                 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        275                 280                 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
    290                 295                 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305                 310                 315                 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                325                 330                 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            340                 345                 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
        355                 360                 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    370                 375                 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
385                 390                 395                 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<212> DNA

<213> Homo sapiens

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<223> sFcRIIB insert with signal sequence

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ggctcctgtt gctgggacac ctgcagctcc cccaaaggct gtgctgaaac tcgagcccca    180

gtggatcaac gtgctccagg aggactctgt gactctgaca tgccggggga ctcacagccc    240
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tgagagcgac tccattcagt ggttccacaa tgggaatctc attcccaccc acacgcagcc 300

cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc agactggcca 360

gaccagcctc agcgaccctg tgcatctgac tgtgctttct gagtggctgg tgctccagac 420

ccctcacctg gagttccagg agggagaaac catcgtgctg aggtgccaca gctggaagga 480

caagcctctg gtcaaggtca cattcttcca gaatggaaaa tccaagaaat tttcccgttc 540

ggatcccaac ttctccatcc cacaagcaaa ccacagtcac agtggtgatt accactgcac 600

aggaaacata ggctacacgc tgttctcatc caagcctgtg accatcactg tccaagctcc 660

cagctcttca cccatggagg agcgcaaatg ttgtgtcgag tgcccaccgt gcccagcacc 720

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ctcccggacc cctgaggtca cgtgcgtggt ggtggacgtg agccacgaag accccgaggt 840

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ggagcagttc aacagcacgt tccgtgtggt cagcgtcctc accgtcgtgc accaggactg 960

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gaaaaccatc tccaaaacca aagggcagcc ccgagaacca caggtgtaca ccctgccccc 1080

atcccgggag gagatgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta 1140

ccccagcgac atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac 1200

cacacctccc atgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga 1260

caagagcagg tggcagcagg ggaacgtctt ctcatgctct gtgatgcatg aggctctgca 1320

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tc 1382

<210> 6

<211> 1418

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIA insert

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ctccacaggt gtccactcca tgcggactga agatctcccc aaggctgtgg tgttcctgga 180

gcctcaatgg tacagggtgc tcgagaagga cagtgtgact ctgaagtgcc agggagccta 240

ctcccctgag gacaattcca cacagtggtt tcacaatgag agcctcatct caagccaggc 300

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ctgcaggggg cttgttggga gtaaaaatgt gtcttcagag actgtgaaca tcaccatcac 660

tcaaggtttg gcagtgtcaa ccatctcatc attctttcca cctgggtacc aagtcgagcg 720

caaatgttgt gtcgagtgcc caccgtgccc agcaccacct gtggcaggac cgtcagtctt 780

cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacgtg 840

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catggaggtg cataatgcca agacaaagcc acgggaggag cagttcaaca gcacgttccg 960

tgtggtcagc gtcctcaccg tcgtgcacca ggactggctg aacggcaagg agtacaagtg 1020

caaggtctcc aacaaaggcc tcccagcccc catcgagaaa accatctcca aaaccaaagg 1080

gcagccccga gaaccacagg tgtacaccct gcccccatcc cgggaggaga tgaccaagaa 1140

ccaggtcagc ctgacctgcc tggtcaaagg cttctacccc agcgacatcg ccgtggagtg 1200

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<211> 1391

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIA-131H

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ggctcctgtt gctgggacac ctgcagctcc cccaaaggct gtgctgaaac ttgagccccc 180

gtggatcaac gtgctccagg aggactctgt gactctgaca tgccaggggg ctcgcagccc 240

tgagagcgac tccattcagt ggttccacaa tgggaatctc attcccaccc acacgcagcc 300

cagctacagg ttcaaggcca acaacaatga cagcggggag tacacgtgcc agactggcca 360

gaccagcctc agcgaccctg tgcatctgac tgtgctttcc gaatggctgg tgctccagac 420

ccctcacctg gagttccagg agggagaaac catcatgctg aggtgccaca gctggaagga 480

caagcctctg gtcaaggtca cattcttcca gaatggaaaa tcccagaaat tctcccattt 540

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aggaaacata ggctacacgc tgttctcatc caagcctgtg accatcactg tccaagtgcc 660

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ctacaagacc acacctccca tgctggactc cgacggctcc ttcttcctct acagcaagct 1260

caccgtggac aagagcaggt ggcagcaggg gaacgtcttc tcatgctctg tgatgcatga 1320

ggctctgcac aaccactaca cacagaagag cctctccctg tctccgggta aatgagtgcg 1380

gccgcgaatt c 1391

<210> 8

<211> 1391

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIA-131R

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<210> 9

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<212> PRT

<213> Homo sapiens

<220>

<223> human FcRIIa

<400> 9

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Trp Leu Leu Gln Pro Leu Thr Val Leu Leu Leu Leu Ala Ser Ala Asp
            20                  25                  30

Ser Gln Ala Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Pro
        35                  40                  45

Trp Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Gln Gly
    50                  55                  60

Ala Arg Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn
65                  70                  75                  80

Leu Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn
                85                  90                  95

Asn Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser
            100                 105                 110

Asp Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr
        115                 120                 125

Pro His Leu Glu Phe Gln Glu Gly Glu Thr Ile Met Leu Arg Cys His
    130                 135                 140

Ser Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly
145                 150                 155                 160

Lys Ser Gln Lys Phe Ser Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln
                165                 170                 175

Ala Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly
            180                 185                 190

Tyr Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Val Pro
        195                 200                 205

Ser Met Gly Ser Ser Ser Pro Met Gly Ile Ile Val Ala Val Val Ile
    210                 215                 220

Ala Thr Ala Val Ala Ala Ile Val Ala Ala Val Val Ala Leu Ile Tyr
225                 230                 235                 240

Cys Arg Lys Lys Arg Ile Ser Ala Asn Ser Thr Asp Pro Val Lys Ala
                245                 250                 255

Ala Gln Phe Glu Pro Pro Gly Arg Gln Met Ile Ala Ile Arg Lys Arg
            260                 265                 270

Gln Leu Glu Glu Thr Asn Asn Asp Tyr Glu Thr Ala Asp Gly Gly Tyr
        275                 280                 285

Met Thr Leu Asn Pro Arg Ala Pro Thr Asp Asp Asp Lys Asn Ile Tyr
    290                 295                 300

Leu Thr Leu Pro Pro Asn Asp His Val Asn Ser Asn Asn
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305 310 315

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<211> 42

<212> DNA

<213> Artificial Sequence

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<223> Primer: SJ45f

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<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> primer: SJ48r

<400> 11
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<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> primer: H009

<400> 12
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<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> primer: SJ27r

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<210> 14

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> primer: SJ47f

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<210> 15

<211> 38

<212> DNA

<213> Artificial Sequence

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<223> primer: SJ20r

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<210> 16

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<212> DNA

<213> Artificial Sequence

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<223> primer: SJ84f

<400> 16

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<210> 17

<211> 35

<212> DNA

<213> Artificial Sequence

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<223> primer: SJ82r

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<210> 18

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer: SJ83f

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<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer: SJ20r

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<210> 20

<211> 83

<212> PRT

<213> Homo sapiens

<220>

<223> Membrane proximal domain of RIIIa

<400> 20

Val His Ile Gly Trp Leu Leu Leu Gln Ala Pro Arg Trp Val Phe Lys
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Glu Glu Asp Pro Ile His Leu Arg Cys His Ser Trp Lys Asn Thr Ala
20 25 30

Leu His Lys Val Thr Tyr Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe
35 40 45

His His Asn Ser Asp Phe Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser
50 55 60

Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly Ser Lys Asn Val Ser Ser
65 70 75 80

Glu Thr Val

<210> 21

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<223> Membrane proximal domain of RIIb

<400> 21

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln
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Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp Lys Pro
20 25 30

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys Phe Ser
35 40 45

Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser His Ser
50 55 60

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
65 70 75

<210> 22

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<223> Membrane proximal domain of RIIa(131R)

<400> 22

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln
1 5 10 15

Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro
20 25 30

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser
35 40 45

Arg Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser
50 55 60

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
65 70 75

<210> 23

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<223> Membrane proximal domain of RIIa(131H)

<400> 23

Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln
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Glu Gly Glu Thr Ile Met Leu Arg Cys His Ser Trp Lys Asp Lys Pro
20 25 30

Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Gln Lys Phe Ser
35 40 45

His Leu Asp Pro Thr Phe Ser Ile Pro Gln Ala Asn His Ser His Ser
50 55 60

Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe
65 70 75

<210> 24

<211> 887

<212> DNA

<213> Homo sapiens

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<223> human FcRIIIa

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gaccctcaag acaaatgacc cccatcccat gggggtaata agagcagtag cagcagcatc 840

tctgaacatt tctctggatt tgcaacccca tcatcctcag gcctctc 887

<210> 25

<211> 254

<212> PRT

<213> Homo sapiens

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<223> human FcRIIIa

<400> 25

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Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

<210> 26

<211> 1393

<212> DNA

<213> Homo sapiens

<220>

<223> human FcRIIB2

<400> 26

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atgcttctgt ggacagctgt gctattcctg gctcctgttg ctgggacacc tgcagctccc 180

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atcgtgctga ggtgccacag ctggaaggac aagcctctgg tcaaggtcac attcttccag 540

aatggaaaat ccaagaaatt ttcccgttcg gatcccaact tctccatccc acaagcaaac 600

cacagtcaca gtggtgatta ccactgcaca ggaaacatag gctacacgct gttctcatcc 660

aagcctgtga ccatcactgt ccaagctccc agctcttcac cgatggggat cattgtggct 720

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cagaaccgta tttagtctcc attgtcttgc attgggattt gagaagaaaa tcagagaggg 960

aagatctggt atttcctggc ctaaattccc cttggaggac agggagatgc tcgagttcca 1020

aaagagaagg tttcttccag agtcatctac ctgagtcctg aagctccctg tcctgaaagc 1080

cacagacaat atggtcccaa ataaccgact gcacctgctg tcttcagctc ttcttgacat 1140

caaggctctt ccgttccaca tccacacagc caatccaatt aatcaaacca ctgttattaa 1200

cagataatag caacttggga aatgcttatg ttacaggtta ccgttgagaa caatcatcta 1260

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<210> 27

<211> 291

<212> PRT

<213> Homo sapiens

<220>

<223> human FcRIIB

<400> 27

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Ala Asp Cys Lys Ser Pro Gln Pro Trp Gly His Met Leu Leu Trp Thr
            20                  25                  30

Ala Val Leu Phe Leu Ala Pro Val Ala Gly Thr Pro Ala Ala Pro Pro
        35                  40                  45

Lys Ala Val Leu Lys Leu Glu Pro Gln Trp Ile Asn Val Leu Gln Glu
    50                  55                  60

Asp Ser Val Thr Leu Thr Cys Arg Gly Thr His Ser Pro Glu Ser Asp

65                  70                  75                  80

Ser Ile Gln Trp Phe His Asn Gly Asn Leu Ile Pro Thr His Thr Gln
                85                  90                  95

Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn Asp Ser Gly Glu Tyr Thr
            100                 105                 110

Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp Pro Val His Leu Thr Val
        115                 120                 125

Leu Ser Glu Trp Leu Val Leu Gln Thr Pro His Leu Glu Phe Gln Glu
    130                 135                 140

Gly Glu Thr Ile Val Leu Arg Cys His Ser Trp Lys Asp Lys Pro Leu
145                 150                 155                 160

Val Lys Val Thr Phe Phe Gln Asn Gly Lys Ser Lys Lys Phe Ser Arg
                165                 170                 175

Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala Asn His Ser His Ser Gly
            180                 185                 190

Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr Thr Leu Phe Ser Ser Lys
        195                 200                 205

Pro Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Gly Ile
    210                 215                 220

Ile Val Ala Val Val Thr Gly Ile Ala Val Ala Ala Ile Val Ala Ala
225                 230                 235                 240

Val Val Ala Leu Ile Tyr Cys Arg Lys Lys Arg Ile Ser Ala Asn Pro
                245                 250                 255

Thr Asn Pro Asp Glu Ala Asp Lys Val Gly Ala Glu Asn Thr Ile Thr
            260                 265                 270

Tyr Ser Leu Leu Met His Pro Asp Ala Leu Glu Glu Pro Asp Asp Gln
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Asn Arg Ile
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<211> 1303

<212> DNA

<213> Homo sapiens

<220>

<223> human FcRIIB1

<400> 28

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ccctcacctg gagttccagg agggagaaac catcgtgctg aggtgccaca gctggaagga 420

caagcctctg gtcaaggtca cattcttcca gaatggaaaa tccaagaaat tttcccgttc 480

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<210> 29

<211> 1466

<212> DNA

<213> Homo sapiens

<220>

<223> human FcRIIB

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<210> 30

<211> 2372

<212> DNA

<213> Homo sapiens

<220>

<223> Human FcRIIa

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<210> 31

<211> 2009

<212> DNA

<213> Homo sapiens

<220>

<223> Human IgG2

<400> 31

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<211> 326

<212> PRT

<213> Homo sapiens

<220>

<223> Human IgG2

<400> 32

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            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65                  70                  75                  80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
            100                 105                 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp

        115                 120                 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    130                 135                 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly

145                 150                 155                 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
                165                 170                 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
            180                 185                 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
        195                 200                 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
    210                 215                 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
```

245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 33

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V1

<400> 33
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ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120

acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180

gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240

gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300

ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360

aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420

tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480

agtaaaaatg tgtcttcaga gactgtgaac atcaccatca ctcaaggtgg cggaggatca 540

gagcgcaaat gttgtgtcga gtgcccaccg tgcccagcac cacctgtggc aggaccgtca 600

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 660

acgtgcgtgg tggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 720

gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 780

ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac 840

aagtgcaagg tctccaacaa aggcctccca gcccccatcg agaaaaccat ctccaaaacc 900

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 960

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1020

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 1080

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1140

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1200

agcctctccc tgtctccggg taaa 1224

<210> 34

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V1

<400> 34

Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln
1 5 10 15

Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
20 25 30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
35 40 45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
50 55 60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65 70 75 80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
85 90 95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His
100 105 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly
115 120 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
130 135 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly
145 150 155 160

Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln Gly
165 170 175

```
Gly Gly Gly Ser Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
            180                 185                 190

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
        195                 200                 205

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
    210                 215                 220

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
225                 230                 235                 240

Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                245                 250                 255

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
            260                 265                 270

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
        275                 280                 285

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
    290                 295                 300

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
305                 310                 315                 320

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
                325                 330                 335

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
            340                 345                 350

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
        355                 360                 365

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
    370                 375                 380

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
385                 390                 395                 400

Ser Leu Ser Leu Ser Pro Gly Lys
                405
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<210> 35

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

<400> 35
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ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120

acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180

gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240

gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300

ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360

aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420

tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480

agtaaaaatg tgtcttcaga gactgtgacc atcaccatca ctcaaggtgg cggaggatca 540

gagcgcaaat gttgtgtcga gtgcccaccg tgcccagcac cacctgtggc aggaccgtca 600

gtcttcctct tccccccaaa acccaaggac accctcatga tctcccggac ccctgaggtc 660

acgtgcgtgg tggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 720

gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 780

ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtac 840

aagtgcaagg tctccaacaa aggcctccca gcccccatcg agaaaaccat ctccaaaacc 900

aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 960

aagaaccagg tcagcctgac ctgcctggtc aaaggcttct accccagcga catcgccgtg 1020

gagtgggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 1080

tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 1140

gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 1200

agcctctccc tgtctccggg taaa 1224

<210> 36

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V2

<400> 36
Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln
 1   5   10   15

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Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
            20                  25                  30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
        35                  40                  45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
    50                  55                  60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65                  70                  75                  80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
                85                  90                  95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His
            100                 105                 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly
        115                 120                 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
    130                 135                 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly
145                 150                 155                 160

Ser Lys Asn Val Ser Ser Glu Thr Val Thr Ile Thr Ile Thr Gln Gly
                165                 170                 175

Gly Gly Gly Ser Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
            180                 185                 190

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
        195                 200                 205

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
    210                 215                 220

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
225                 230                 235                 240

Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
                245                 250                 255

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
            260                 265                 270

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
        275                 280                 285

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
    290                 295                 300

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
305                 310                 315                 320

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
                325                 330                 335
```

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
340 345 350

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
355 360 365

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
370 375 380

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
385 390 395 400

Ser Leu Ser Leu Ser Pro Gly Lys
405

<210> 37

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 37
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ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120

acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180

gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240

gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300

ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360

aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420

tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480

agtaaaaatg tgtcttcaga gactgtgaac atcactgtcc aagctcccag ctcttcaccc 540

atggaggagc gcaaatgttg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 600

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 660

gaggtcacgt gcgtggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 720

tacgtggacg gcatggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 780

agcacgttcc gtgtggtcag cgtcctcacc gtcgtgcacc aggactggct gaacggcaag 840

gagtacaagt gcaaggtctc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc 900

aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 960

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1020

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1080

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1140

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1200

cagaagagcc tctccctgtc tccgggtaaa 1230

<210> 38

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V3

<400> 38

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Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln
 1               5                  10                  15

Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
            20                  25                  30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
        35                  40                  45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
    50                  55                  60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65                  70                  75                  80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
                85                  90                  95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His
            100                 105                 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly
        115                 120                 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
    130                 135                 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly
145                 150                 155                 160

Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Val Gln Ala Pro
                165                 170                 175
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Ser Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro
            180                 185                 190

Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro
        195                 200                 205

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    210                 215                 220

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp
225                 230                 235                 240

Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                245                 250                 255

Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val
            260                 265                 270

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        275                 280                 285

Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly
    290                 295                 300

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
305                 310                 315                 320

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                325                 330                 335

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            340                 345                 350

Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
        355                 360                 365

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    370                 375                 380

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
385                 390                 395                 400

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                405                 410
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<210> 39

<211> 1230

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V4

<400> 39
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ctcgagaagg acagtgtgac tctgaagtgc cagggagcct actcccctga ggacaattcc 120

acacagtggt ttcacaatga gagcctcatc tcaagccagg cctcgagcta cttcattgac 180

gctgccacag tcgacgacag tggagagtac aggtgccaga caaacctctc caccctcagt 240

gacccggtgc agctagaagt ccatatcggc tggctgttgc tccaggcccc tcggtgggtg 300

ttcaaggagg aagaccctat tcacctgagg tgtcacagct ggaagaacac tgctctgcat 360

aaggtcacat atttacagaa tggcaaaggc aggaagtatt ttcatcataa ttctgacttc 420

tacattccaa aagccacact caaagacagc ggctcctact tctgcagggg gcttgttggg 480

agtaaaaatg tgtcttcaga gactgtgacc atcactgtcc aagctcccag ctcttcaccc 540

atggaggagc gcaaatgttg tgtcgagtgc ccaccgtgcc cagcaccacc tgtggcagga 600

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 660

gaggtcacgt gcgtggtggt ggacgtgagc cacgaagacc ccgaggtcca gttcaactgg 720

tacgtggacg gcatggaggt gcataatgcc aagacaaagc cacgggagga gcagttcaac 780

agcacgttcc gtgtggtcag cgtcctcacc gtcgtgcacc aggactggct gaacggcaag 840

gagtacaagt gcaaggtctc caacaaaggc ctcccagccc ccatcgagaa aaccatctcc 900

aaaaccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 960

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctaccc cagcgacatc 1020

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac acctcccatg 1080

ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 1140

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacaca 1200

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<210> 40

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIIAG2-V4

<400> 40

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Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro Gln
 1               5                  10                  15

Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln Gly
            20                  25                  30

Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu Ser
        35                  40                  45

Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr Val
    50                  55                  60

Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu Ser
65                  70                  75                  80

Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln Ala
                85                  90                  95

Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys His
            100                 105                 110

Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn Gly
        115                 120                 125

Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro Lys
    130                 135                 140

Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val Gly
145                 150                 155                 160

Ser Lys Asn Val Ser Ser Glu Thr Val Thr Ile Thr Val Gln Ala Pro
                165                 170                 175

Ser Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro
            180                 185                 190

Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro
        195                 200                 205

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    210                 215                 220

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp
225                 230                 235                 240

Tyr Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                245                 250                 255

Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val
            260                 265                 270

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        275                 280                 285

Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly
    290                 295                 300

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
305                 310                 315                 320
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Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
325 330 335

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
340 345 350

Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
355 360 365

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
370 375 380

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
385 390 395 400

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
405 410

<210> 41

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<223> sFcRIIBG2-N297Q

<400> 41
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gccaacaaca atgacagcgg ggagtacacg tgccagactg gccagaccag cctcagcgac 240

cctgtgcatc tgactgtgct ttctgagtgg ctggtgctcc agacccctca cctggagttc 300

caggagggag aaaccatcgt gctgaggtgc cacagctgga aggacaagcc tctggtcaag 360

gtcacattct tccagaatgg aaaatccaag aaattttccc gttcggatcc caacttctcc 420

atcccacaag caaaccacag tcacagtggt gattaccact gcacaggaaa cataggctac 480

acgctgttct catccaagcc tgtgaccatc actgtccaag ctcccagctc ttcacccatg 540

gaggagcgca aatgttgtgt cgagtgccca ccgtgcccag caccacctgt ggcaggaccg 600

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag 660

gtcacgtgcg tggtggtgga cgtgagccac gaagaccccg aggtccagtt caactggtac 720

gtggacggca tggaggtgca taatgccaag acaaagccac gggaggagca gttccagagc 780

acgttccgtg tggtcagcgt cctcaccgtc gtgcaccagg actggctgaa cggcaaggag 840

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accaaagggc agccccgaga accacaggtg tacaccctgc ccccatcccg ggaggagatg 960

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gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacacc tcccatgctg 1080

gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1140

caggggaacg tcttctcatg ctctgtgatg catgaggctc tgcacaacca ctacacacag 1200

aagagcctct ccctgtctcc gggtaaa 1227

<210> 42

<211> 409

<212> PRT

<213> Homo sapiens

<220>

<223> sFcRIIBG2-N297Q

<400> 42

Thr Pro Ala Ala Pro Pro Lys Ala Val Leu Lys Leu Glu Pro Gln Trp
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Ile Asn Val Leu Gln Glu Asp Ser Val Thr Leu Thr Cys Arg Gly Thr
20 25 30

His Ser Pro Glu Ser Asp Ser Ile Gln Trp Phe His Asn Gly Asn Leu
35 40 45

Ile Pro Thr His Thr Gln Pro Ser Tyr Arg Phe Lys Ala Asn Asn Asn
50 55 60

Asp Ser Gly Glu Tyr Thr Cys Gln Thr Gly Gln Thr Ser Leu Ser Asp
65 70 75 80

Pro Val His Leu Thr Val Leu Ser Glu Trp Leu Val Leu Gln Thr Pro
85 90 95

His Leu Glu Phe Gln Glu Gly Glu Thr Ile Val Leu Arg Cys His Ser
100 105 110

Trp Lys Asp Lys Pro Leu Val Lys Val Thr Phe Phe Gln Asn Gly Lys
115 120 125

Ser Lys Lys Phe Ser Arg Ser Asp Pro Asn Phe Ser Ile Pro Gln Ala
130 135 140

Asn His Ser His Ser Gly Asp Tyr His Cys Thr Gly Asn Ile Gly Tyr
145 150 155 160

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Thr Leu Phe Ser Ser Lys Pro Val Thr Ile Thr Val Gln Ala Pro Ser
                165                 170                 175

Ser Ser Pro Met Glu Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
            180                 185                 190

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        195                 200                 205

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    210                 215                 220

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
225                 230                 235                 240

Val Asp Gly Met Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                245                 250                 255

Gln Phe Gln Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
            260                 265                 270

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        275                 280                 285

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
    290                 295                 300

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
305                 310                 315                 320

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                325                 330                 335

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            340                 345                 350

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
        355                 360                 365

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
    370                 375                 380

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
385                 390                 395                 400

Lys Ser Leu Ser Leu Ser Pro Gly Lys
                405
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Gly Tyr Gln Val
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Phe Phe Pro Pro Gly Tyr Gln Val
            20

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Val Thr Ile Thr Val Gln Ala Pro Ser Ser Ser Pro Met Glu
1 5 10